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☐	L14	2000	8
☐	L13	2000	55
☐	L12	L11 same (deconvolute or deconvolution or track or tracking or identify or identification)	55
☐	L11	L10 same combinatorial	198
☐	L10	split adj2 (pool or combine)	639
☐	L9	"split and pool" or "split and combine"	0
☐	L8	combinatorial same (("split and pool") or ("split and combine"))	0
☐	L7	combinatorial same ("split and pool" or "split and combine")	0
☐	L6	combinatorial same ((split and pool) or (split and combine))	318
☐	L5	2000	93
☐	L4	l2 same (deconvolut$ or track$ or identif$)	215
☐	L3	L2 same (deconvolut$ or track$)	60
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☐	L1	combinatorial same ((split and pool) or (split and combine))	318

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NEWS 5	SEP 29	DISSABS now available on STN
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NEWS 7	OCT 21	BIOSIS file reloaded and enhanced
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=> s combinatorial and ((split and pool) or (split and combine))
L1 49 COMBINATORIAL AND ((SPLIT AND POOL) OR (SPLIT AND COMBINE))

=> s l1 and py<2000
L2 12 L1 AND PY<2000

=> duplicate remove l2
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
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PROCESSING COMPLETED FOR L2
L3 7 DUPLICATE REMOVE L2 (5 DUPLICATES REMOVED)

=> d 1-7 bib ab

L3 ANSWER 1 OF 7 MEDLINE on STN
AN 1999001046 MEDLINE
DN PubMed ID: 9784868
TI A metathetical cycloaddition-cycloreversion approach to the formation of furan scaffold libraries.
AU Whitehouse D L; Nelson K H Jr; Savinov S N; Lowe R S; Austin D J
CS Department of Chemistry, Yale University, New Haven, CT 06520-8107, USA.
SO Bioorganic & medicinal chemistry, **(1998 Aug)** 6 (8) 1273-82.
Journal code: 9413298. ISSN: 0968-0896.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199901
ED Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19990107
AB A general cycloaddition-cycloreversion metathesis procedure for the selective formation of a furan-based template-directed scaffold is described. In addition, features relative to library construction, such as the chemoselective nature of dipole formation, are discussed. Through the investigation of the temperature sensitive cleavage step, the furan synthesis was found to be accelerated by aqueous medium at physiological temperature leading to pure product from the solid-phase under biologically relevant conditions. The chemoselective nature of the rhodium(II) mediated cycloaddition allowed the selective formation of a key dipole intermediate, in the presence of a number of carbeneactive functional groups, to facilitate the **split-pool combinatorial** synthesis of a small library of compounds.

L3 ANSWER 2 OF 7 MEDLINE on STN DUPLICATE 1
AN 1998089196 MEDLINE

DN PubMed ID: 9427663
TI Small molecule-dependent genetic selection in stochastic nanodroplets as a means of detecting protein-ligand interactions on a large scale.
AU Borchardt A; Liberles S D; Biggar S R; Crabtree G R; Schreiber S L
CS Howard Hughes Medical Institute, Department of Chemistry and Chemical Biology, Harvard University, Cambridge, MA 02138, USA.
SO Chemistry & biology, **(1997 Dec)** 4 (12) 961-8.
Journal code: 9500160. ISSN: 1074-5521.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199803
ED Entered STN: 19980312
Last Updated on STN: 19990129
Entered Medline: 19980305
AB BACKGROUND: Understanding the cellular role of a protein often requires a means of altering its function, most commonly by mutating the gene encoding the protein. Alternatively, protein function can be altered directly using a small molecule that binds to the protein, but no general method exists for the systematic discovery of small molecule ligands. **Split-pool** synthesis provides a means of synthesizing vast numbers of small molecules. Synthetic chemists will soon be able to synthesize natural product-like substances by this method, so compatible screening methods that detect the activity of minute quantities of molecules among many inactive ones will be in demand. RESULTS: We describe two advances towards achieving the above goals. First, a technique is described that uses a simple spray gun to create 5000-8000 droplets randomly, each having a volume of 50-200 nanoliters. The individual 'nanodroplets' contain a controlled number of cells and many also contain individual synthesis beads. As small molecules can be photochemically released from the beads in a time-dependent manner, the concentration of ligands that the cells are exposed to can be controlled. The spatial segregation of nanodroplets prevents the mixing of compounds from other beads so the effects of each molecule can be assayed individually. Second, a small molecule-dependent genetic selection involving engineered budding yeast cells was used to detect intracellular protein-ligand interactions in nanodroplets. CONCLUSIONS: The technique described here should facilitate the discovery of new cell-permeable ligands, especially when combined with a positive selection assay that detects intracellular binding of small molecules to proteins. Using 'anchored **combinatorial** libraries', it may be possible to screen entire libraries of natural product-like molecules against the entire collection of proteins encoded within cDNA libraries in a single experiment.

L3 ANSWER 3 OF 7 MEDLINE on STN
AN 1998141065 MEDLINE
DN PubMed ID: 9527475
TI Composition and purity of **combinatorial** aryl ether collections analyzed by electrospray mass spectrometry.
AU Haap W J; Metzger J W; Kempter C; Jung G
CS Institute of Organic Chemistry, University of Tubingen, Germany.
SO Molecular diversity, **(1997)** 3 (1) 29-41.
Journal code: 9516534. ISSN: 1381-1991.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199804
ED Entered STN: 19980410
Last Updated on STN: 20030123

Entered Medline: 19980402

AB Electrospray mass spectrometry (ESI-MS), tandem mass spectrometry and on-line RP-HPLC-ESI-MS were used to evaluate the composition and purity of three different aryl ether mixtures consisting of 10 and 45 aryl ethers synthesized on solid support by Williamson etherification. The libraries feature two potential pharmacophores connected with three different spacers and serve as models for a detailed component analysis. Individual members of the library and by-products were identified rapidly and conveniently by product ion scans. Compound collections obtained by two different synthetic methods, the **split/combine** approach and the premix method, showed different mass distributions in the ESI-MS spectra. Some components were not detected in direct ESI-MS measurements, but were found by MS/MS experiments. Precursor ion and constant neutral loss scans allowed the identification of components with common structural features.

L3 ANSWER 4 OF 7 MEDLINE on STN DUPLICATE 2
AN 97380411 MEDLINE
DN PubMed ID: 9237200
TI **Combinatorial** synthesis of small-molecule libraries using 3-amino-5-hydroxybenzoic acid.
AU Dankwardt S M; Phan T M; Krstenansky J L
CS Syntex Discovery Research, Chemical Research and Development, Palo Alto, CA 94304, USA.
SO Molecular diversity, **(1996 Feb)** 1 (2) 113-20.
Journal code: 9516534. ISSN: 1381-1991.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199709
ED Entered STN: 19971008
Last Updated on STN: 19971008
Entered Medline: 19970923

AB A non-peptide library of 2001 compounds has been prepared utilizing solid-phase techniques. The **split/combine** method was demonstrated to work well to form mixtures of compounds based on 3-amino-5-hydroxybenzoic acid as a core structure. The benzoic acid of the core structure served as the attachment point for the resin and the amino and hydroxy positions were variably substituted.

L3 ANSWER 5 OF 7 MEDLINE on STN DUPLICATE 3
AN 97381305 MEDLINE
DN PubMed ID: 9238637
TI Design, synthesis and use of binary encoded synthetic chemical libraries.
AU Baldwin J J
CS Pharmacopeia Inc., Princeton, NJ 08540, USA.
SO Molecular diversity, **(1996 Oct)** 2 (1-2) 81-8. Ref: 26
Journal code: 9516534. ISSN: 1381-1991.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199708
ED Entered STN: 19970902
Last Updated on STN: 19980206
Entered Medline: 19970821

AB With the advent of **combinatorial** chemistry a new paradigm is evolving in the field of drug discovery. The approach is based on an integration of chemistry, high-throughput screening and automation

engineering. The chemistry arm is usually based on solid-phase synthesis technology as the preferred approach to library construction. One of the most powerful of the solid-phase methods is encoded **split** synthesis, in which the reaction history experience by each polymeric bead is unambiguously recorded. This **split**-and-**pool** approach, employing chemically robust tags, was used to construct a 85,000-membered dihydrobenzopyran library.

L3 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 4
AN 2001561539 MEDLINE
DN PubMed ID: 11607586
TI Sample size determination in **combinatorial** chemistry.
AU Zhao P L; Zambias R; Bolognese J A; Boulton D; Chapman K
CS Department of Biometrics Research, Merck Research Laboratories, Rahway, NJ 07065, USA.
SO Proceedings of the National Academy of Sciences of the United States of America, **(1995 Oct 24)** 92 (22) 10212-6.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS PUBMED-NOT-MEDLINE
EM 200112
ED Entered STN: 20011022
Last Updated on STN: 20020124
Entered Medline: 20011228
AB **Combinatorial** chemistry is gaining wide appeal as a technique for generating molecular diversity. Among the many **combinatorial** protocols, the **split**/recombine method is quite popular and particularly efficient at generating large libraries of compounds. In this process, polymer beads are equally divided into a series of **pools** and each **pool** is treated with a unique fragment; then the beads are recombined, mixed to uniformity, and redivided equally into a new series of **pools** for the subsequent couplings. The deviation from the ideal equimolar distribution of the final products is assessed by a special overall relative error, which is shown to be related to the Pearson statistic. Although the **split**/recombine sampling scheme is quite different from those used in analysis of categorical data, the Pearson statistic is shown to still follow a chi2 distribution. This result allows us to derive the required number of beads such that, with 99% confidence, the overall relative error is controlled to be less than a pregiven tolerable limit L1. In this paper, we also discuss another criterion, which determines the required number of beads so that, with 99% confidence, all individual relative errors are controlled to be less than a pregiven tolerable limit L2 (0 < L2 < 1).

L3 ANSWER 7 OF 7 MEDLINE on STN DUPLICATE 5
AN 95062280 MEDLINE
DN PubMed ID: 7972077
TI Recursive deconvolution of **combinatorial** chemical libraries.
AU Erb E; Janda K D; Brenner S
CS Department of Molecular Biology, Scripps Research Institute, La Jolla, CA 92037.
SO Proceedings of the National Academy of Sciences of the United States of America, **(1994 Nov 22)** 91 (24) 11422-6.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199412
ED Entered STN: 19950110

Last Updated on STN: 19950110
Entered Medline: 19941227

AB A recursive strategy that solves for the active members of a chemical library is presented. A pentapeptide library with an alphabet of Gly, Leu, Phe, and Tyr (1024 members) was constructed on a solid support by the method of **split** synthesis. One member of this library (NH2-Tyr-Gly-Gly-Phe-Leu) is a native binder to a beta-endorphin antibody. A variation of the **split** synthesis approach is used to build the **combinatorial** library. In four vials, a member of the library's alphabet is coupled to a solid support. After each coupling, a portion of the resin from each of the four reaction vials was set aside and catalogued. The solid support from each vial is then combined, mixed, and redivided. The steps of (i) coupling, (ii) saving and cataloging, and (iii) randomizing were repeated until a pentapeptide library was obtained. The four pentapeptide libraries where the N-terminal amino acid is defined were screened against the beta-endorphin antibody and quantitated via an ELISA. The amino acid of the four **pools** that demonstrated the most binding was then coupled to the four tetrapeptide partial libraries that had been set aside and catalogued during the **split** synthesis. This recursive deconvolution was repeated until the best binders were deduced. Besides the anticipated native binder, two other members of the library displayed significant binding. This recursive method of deconvolution does not use a molecular tag, requires only one **split** synthesis, and can be applied to the deconvolution of nonlinear small-molecule **combinatorial** libraries and linear oligomeric **combinatorial** libraries, since it is based only on the procedure of the synthesis.

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